

## RAW SEQUENCE LISTING

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Application Serial Number: 10/006,305A  
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PATENT APPLICATION: US/10/006,305A

DATE: 10/29/2004

TIME: 13:08:30

Input Set : A:\41673292.app

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3 <110> APPLICANT: PRUSSAK, CHARLES E.
4     KIPPS, THOMAS J.
5     CANTWELL, MARK J.
7 <120> TITLE OF INVENTION: NOVEL CHIMERIC TNF LIGANDS
9 <130> FILE REFERENCE: 041673-2092
11 <140> CURRENT APPLICATION NUMBER: 10/006,305A
12 <141> CURRENT FILING DATE: 2001-12-06
14 <160> NUMBER OF SEQ ID NOS: 8
16 <170> SOFTWARE: PatentIn Ver. 3.2
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 771
20 <212> TYPE: DNA
21 <213> ORGANISM: Artificial Sequence
23 <220> FEATURE:
24 <223> OTHER INFORMATION: Description of Artificial Sequence: Chimeric DNA construct
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26     III of hCD154
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30 atgaaaattt ttatgtattt acttactgtt tttcttatca cccagatgat tgggtcagca 120
31 ctttttgctg tgtatcttca tagaaggctg gacaagatag aagatgaaag gaatcttcat 180
32 gaagattttg tattcatgaa aacgatacag agatgcaaca caggagaaag atccttatcc 240
33 ttactgaact gtgaggagat taaaagccag tttgaaggct ttgtgaagga tataatgtta 300
34 aacaaagagg agacgaagaa agatgaggat cctgtagccc atgtttagc aaacctcaa 360
35 gctgaggggc agctccagt gctgaaccgc cgggccaatg ccctcctggc caatggcgtg 420
36 gagctgagag ataaccagct ggtggtgcca tcagagggcc tgtacctcat ctactcccag 480
37 gtcctcttca agggccaagg ctgcccctcc acccatgtgc tcctcaccca caccatcagc 540
38 cgcacgcgcg tctctacca gaccaaggct aacctcctct ctgccatcaa gagcccctgc 600
39 cagagggaga cccagaggg ggctgaggcc aagccctggt atgagcccat ctatctggga 660
40 ggggtcttcc agctggagaa ggtgaccga ctcagcgtg agatcaatcg gcccgactat 720
41 ctcgactttg cggagtctg gcaggtctac tttggaatca ttgctctgtg a 771
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45 <211> LENGTH: 580
46 <212> TYPE: DNA
47 <213> ORGANISM: Artificial Sequence
49 <220> FEATURE:
50 <223> OTHER INFORMATION: Description of Artificial Sequence: Chimeric DNA construct
51     comprising Domain IV of hTNFa linked to Domains I, II, and
52     III of hCD70
54 <400> SEQUENCE: 2
55 atgccggagg aggggttcggg ctgctcggtg cggcgcaggc cctatgggtg cgtcctgcgg 60
56 gctgctttgg tccattggt cgcgggcttg gtgatctgcc tcgtggtgtg catccagcgc 120
57 ttgcacagc ctgcggatcc tgtagcccat gttgtagcaa accctcaagc tgaggggcag 180

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58 ctccagtggc tgaaccgccg ggccaatgcc ctcttgccca atggcgtgga gctgagagat 240
59 aaccagctgg tgggtgccatc agagggcctg tacctcatct actcccaggt cctcttcaag 300
60 ggccaaggct gccctccac ccatgtgctc ctacccaca ccatcagccg catcgccgtc 360
61 tcctaccaga ccaaggctcaa cctcctctct gccatcaaga gccctgcca gagggagacc 420
62 ccagaggggg ctgaggccaa gccctggtat gagcccatct atctgggagg ggtcttccag 480
63 ctggagaagg gtgaccgact cagcgtgag atcaatcggc ccgactatct cgactttgcg 540
64 gagtctgggc aggtctactt tggaatcatc gctctgtgaa 580
67 <210> SEQ ID NO: 3
68 <211> LENGTH: 837
69 <212> TYPE: DNA
70 <213> ORGANISM: Artificial Sequence
72 <220> FEATURE:
73 <223> OTHER INFORMATION: Description of Artificial Sequence: Chimeric DNA construct
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75 of hFasL
77 <400> SEQUENCE: 3
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79 tctccctggg cccctccagg cacagttctt ccctgtccaa cctctgtgcc cagaaggcct 120
80 ggtcaaagga ggccaccacc accaccgcca ccgccaccac taccacctcc gccgccgccg 180
81 ccaccactgc ctccactacc gctgccaccc ctgaagaaga gaggaacca cagcacaggc 240
82 ctgtgtctcc ttgtgatgtt tttcatgggt ctggttgctt tggtaggatt gggcctgggg 300
83 atgtttcagc tcttccacct acagaaggag ctggcagaac tccgagagtc taccagccag 360
84 atgcacacag catcatcttt ggagaagcaa gcggatcctg tagcccatgt ttagcaaac 420
85 cctcaagctg aggggcagct ccagtggctg aaccgccggg ccaatgccct cctggccaat 480
86 ggcgtggagc tgagagataa ccagctggtg gtgccatcag agggcctgta cctcatctac 540
87 tcccaggtcc tcttcaaggg ccaaggctgc cctccacccc atgtgctcct caccacacc 600
88 atcagccgca tcgccgtctc ctaccagacc aaggctcaacc tcctctctgc catcaagagc 660
89 ccctgccaga gggagacccc agagggggct gaggccaagc cctggtatga gcccatctat 720
90 ctgggagggg tcttccagct ggagaagggt gaccgactca gcgctgagat caatcgcccc 780
91 gactatctcg actttgcgga gtctgggcag gtctactttg gaatcattgc tctgtga 837
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94 <211> LENGTH: 813
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96 <213> ORGANISM: Artificial Sequence
98 <220> FEATURE:
99 <223> OTHER INFORMATION: Description of Artificial Sequence: Chimeric DNA construct
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101 III of hTRAIL
103 <400> SEQUENCE: 4
104 atggctatga tggaggtcca ggggggaccc agcctgggac agacctgcgt gctgatcgctg 60
105 atcttcacag tgctcctgca gtctctctgt gtggctgtaa cttacgtgta ctttaccac 120
106 gagctgaagc agatgcagga caagtactcc aaaagtggca ttgcttggtt cttaaaagaa 180
107 gatgacagtt attgggaccc caatgacgaa gagagtatga acagcccctg ctggcaagtc 240
108 aagtggcaac tccgtcagct cgttagaaag atgattttga gaacctctga ggaaaccatt 300
109 tctacagttc aagaaaagca acaaaatatt tctcccctag tgagagaaag aggtcctcag 360
110 agagtagcgg atcctgtagc ccatgttgta gcaaacctc aagctgaggg gcagctccag 420
111 tggctgaacc gccgggcca tgcctcctc gccaatggcg tggagctgag agataaccag 480
112 ctggtggtgc catcagaggg cctgtacctc atctactccc aggtcctctt caagggcca 540
113 ggctgccccct ccacccatgt gctcctcacc cacaccatca gccgcacgc cgtctcctac 600

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114 cagaccaagg tcaacctcct ctctgccatc aagagcccct gccagagggga gaccccagag 660
115 ggggctgagg ccaagccctg gtatgagccc atctatcttg gaggggtctt ccagctggag 720
116 aagggtgacc gactcagcgc tgagatcaat cggcccgcact atctcgactt tgcggagtct 780
117 gggcaggtct actttggaat cattgctctg tga 813
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121 <211> LENGTH: 256
122 <212> TYPE: PRT
123 <213> ORGANISM: Artificial Sequence
125 <220> FEATURE:
126 <223> OTHER INFORMATION: Description of Artificial Sequence: Chimeric TNFa
127 polypeptide encoded by the DNA sequence of SEQ ID NO:1
129 <400> SEQUENCE: 5
130 Met Ile Glu Thr Tyr Asn Gln Thr Ser Pro Arg Ser Ala Ala Thr Gly
131 1 5 10 15
133 Leu Pro Ile Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu
134 20 25 30
136 Ile Thr Gln Met Ile Gly Ser Ala Leu Phe Ala Val Tyr Leu His Arg
137 35 40 45
139 Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val
140 50 55 60
142 Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser
143 65 70 75 80
145 Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys
146 85 90 95
148 Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Asp Glu Asp Pro Val
149 100 105 110
151 Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu
152 115 120 125
154 Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp
155 130 135 140
157 Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln
158 145 150 155 160
160 Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr
161 165 170 175
163 His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu
164 180 185 190
166 Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala
167 195 200 205
169 Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln
170 210 215 220
172 Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr
173 225 230 235 240
175 Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
176 245 250 255
182 <210> SEQ ID NO: 6
183 <211> LENGTH: 192
184 <212> TYPE: PRT
185 <213> ORGANISM: Artificial Sequence
187 <220> FEATURE:

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188 <223> OTHER INFORMATION: Description of Artificial Sequence: Chimeric TBFa
189     polypeptide encoded by the DNA sequence of SEQ ID NO:2
191 <400> SEQUENCE: 6
192 Met Pro Glu Glu Gly Ser Gly Cys Ser Val Arg Arg Arg Pro Tyr Gly
193   1           5           10           15
195 Cys Val Leu Arg Ala Ala Leu Val Pro Leu Val Ala Gly Leu Val Ile
196           20           25           30
198 Cys Leu Val Val Cys Ile Gln Arg Phe Ala Gln Ala Ala Asp Pro Val
199           35           40           45
201 Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu
202           50           55           60
204 Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp
205   65           70           75           80
207 Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln
208           85           90           95
210 Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr
211           100          105          110
213 His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu
214           115          120          125
216 Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala
217           130          135          140
219 Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln
220  145          150          155          160
222 Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr
223           165          170          175
225 Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
226           180          185          190
232 <210> SEQ ID NO: 7
233 <211> LENGTH: 278
234 <212> TYPE: PRT
235 <213> ORGANISM: Artificial Sequence
237 <220> FEATURE:
238 <223> OTHER INFORMATION: Description of Artificial Sequence: Chimeric TNFa
239     polypeptide encoded by the DNA sequence of SEQ ID NO:3
241 <400> SEQUENCE: 7
242 Met Gln Gln Pro Phe Asn Tyr Pro Tyr Pro Gln Ile Tyr Trp Val Asp
243   1           5           10           15
245 Ser Ser Ala Ser Ser Pro Trp Ala Pro Pro Gly Thr Val Leu Pro Cys
246           20           25           30
248 Pro Thr Ser Val Pro Arg Arg Pro Gly Gln Arg Arg Pro Pro Pro Pro
249           35           40           45
251 Pro Pro Pro Pro Pro Leu Pro Pro Pro Pro Pro Pro Pro Pro Leu Pro
252           50           55           60
254 Pro Leu Pro Leu Pro Pro Leu Lys Lys Arg Gly Asn His Ser Thr Gly
255   65           70           75           80
257 Leu Cys Leu Leu Val Met Phe Phe Met Val Leu Val Ala Leu Val Gly
258           85           90           95
260 Leu Gly Leu Gly Met Phe Gln Leu Phe His Leu Gln Lys Glu Leu Ala
261           100          105          110

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263 Glu Leu Arg Glu Ser Thr Ser Gln Met His Thr Ala Ser Ser Leu Glu
264      115      120      125
266 Lys Gln Ala Asp Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu
267      130      135      140
269 Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn
270 145      150      155      160
272 Gly Val Glu Leu Arg Asp Asn Glu Leu Val Val Pro Ser Glu Gly Leu
273      165      170      175
275 Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser
276      180      185      190
278 Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr
279      195      200      205
281 Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg
282      210      215      220
284 Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr
285 225      230      235      240
287 Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu
288      245      250      255
290 Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr
291      260      265      270
293 Phe Gly Ile Ile Ala Leu
294      275
297 <210> SEQ ID NO: 8
298 <211> LENGTH: 270
299 <212> TYPE: PRT
300 <213> ORGANISM: Artificial Sequence
302 <220> FEATURE:
303 <223> OTHER INFORMATION: Description of Artificial Sequence: Chimeric TNFa
304      polypeptide encoded by the DNA sequence of SEQ ID NO:4
306 <400> SEQUENCE: 8
307 Met Ala Met Met Glu Val Gln Gly Gly Pro Ser Leu Gly Gln Thr Cys
308 1      5      10      15
310 Val Leu Ile Val Ile Phe Thr Val Leu Leu Gln Ser Leu Cys Val Ala
311      20      25      30
313 Val Thr Tyr Val Tyr Phe Thr Asn Glu Leu Lys Gln Met Gln Asp Lys
314      35      40      45
316 Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser Tyr
317      50      55      60
319 Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln Val
320 65      70      75      80
322 Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr Ser
323      85      90      95
325 Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro
326      100      105      110
328 Leu Val Arg Glu Arg Glu Pro Gln Arg Val Ala Asp Pro Val Ala His
329      115      120      125
331 Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg
332      130      135      140
334 Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln

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**VERIFICATION SUMMARY**

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